

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/162,407DATE: 12/27/93
TIME: 12:37:42

INPUT SET: S1194.raw

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia

(ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
(B) STREET: 51 University Street
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: US
(F) ZIP: 98101

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Apple Macintosh
(C) OPERATING SYSTEM: Macintosh 7.0.1
(D) SOFTWARE: Microsoft Word, Version #5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: -to be assigned-
(B) FILING DATE: December 3, 1993
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/111,758
(B) FILING DATE: August 25, 1993
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/106,463
(B) FILING DATE: August 12, 1993
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/068,394
(B) FILING DATE: May 24, 1993
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Malaska, Stephen L.
(B) REGISTRATION NUMBER: 32,655
(C) REFERENCE/DOCKET NUMBER: 2813-C

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 587-0430

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52 (B) TELEFAX: (206) 233-0644
53 (C) TELEX: 756822
54

(2) INFORMATION FOR SEQ ID NO:1:

56 (i) SEQUENCE CHARACTERISTICS:
57 (A) LENGTH: 879 base pairs
58 (B) TYPE: nucleic acid
59 (C) STRANDEDNESS: single
60 (D) TOPOLOGY: linear
61

62 (ii) MOLECULE TYPE: cDNA to mRNA
63

64 (iii) HYPOTHETICAL: NO
65

66 (iv) ANTI-SENSE: NO
67

68 (ix) FEATURE:
69 (A) NAME/KEY: misc_feature
70 (B) LOCATION: 1..25
71

72 (ix) FEATURE:
73 (A) NAME/KEY: misc_feature
74 (B) LOCATION: 855..879
75

76 (ix) FEATURE:
77 (A) NAME/KEY: CDS
78 (B) LOCATION: 57..752
79

80

81

82 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
83

84 GTCGACTGGA ACGAGACGAC CTGCTCTGTC ACAGGCATGA GGGGTCCCCG GCAGAG 56

85

86 ATG ACA GTG CTG GCG CCA GCC TGG AGC CCA AAT TCC TCC CTG TTG CTG 104

87 Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu

88 1 5 10 15

89

90 CTG TTG CTG CTG CTG AGT CCT TGC CTG CGG GGG ACA CCT GAC TGT TAC 152

91 Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr

92 20 25 30

93 TTC AGC CAC AGT CCC ATC TCC TCC AAC TTC AAA GTG AAG TTT AGA GAG 200

94 Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu

95 35 40 45

96

97 TTG ACT GAC CAC CTG CTT AAA GAT TAC CCA GTC ACT GTG GCC GTC AAT 248

98 Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn

99 50 55 60

100

101 CTT CAG GAC GAG AAG CAC TGC AAG GCC TTG TGG AGC CTC TTC CTA GCC 296

102 Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala

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103	65		70		75		80	
104								
105	CAG CGC TGG ATA GAG CAA CTG AAG ACT GTG GCA GGG TCT AAG ATG CAA	344						
106	Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln							
107	85 90 95							
108								
109	ACG CTT CTG GAG GAC GTC AAC ACC GAG ATA CAT TTT GTC ACC TCA TGT	392						
110	Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys							
111	100 105 110							
112								
113	ACC TTC CAG CCC CTA CCA GAA TGT CTG CGA TTC GTC CAG ACC AAC ATC	440						
114	Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile							
115	115 120 125							
116								
117	TCC CAC CTC CTG AAG GAC ACC TGC ACA CAG CTG CTT GCT CTG AAG CCC	488						
118	Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro							
119	130 135 140							
120								
121	TGT ATC GGG AAG GCC TGC CAG AAT TTC TCT CGG TGC CTG GAG GTG CAG	536						
122	Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln							
123	145 150 155 160							
124								
125	TGC CAG CCG GAC TCC TCC ACC CTG CTG CCC CCA AGG AGT CCC ATA GCC	584						
126	Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala							
127	165 170 175							
128								
129	CTA GAA GCC ACG GAG CTC CCA GAG CCT CGG CCC AGG CAG CTG TTG CTC	632						
130	Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu							
131	180 185 190							
132								
133	CTG CTG CTG CTG CTG CCT CTC ACA CTG GTG CTG CTG GCA GCC GCC TGG	680						
134	Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp							
135	195 200 205							
136								
137	GGC CTT CGC TGG CAA AGG GCA AGA AGG AGG GGG GAG CTC CAC CCT GGG	728						
138	Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly							
139	210 215 220							
140								
141	GTG CCC CTC CCC TCC CAT CCC TAGGATTCTGA GCCTTGTGCA TCGTTGACTC	779						
142	Val Pro Leu Pro Ser His Pro							
143	225 230							
144								
145	AGCCAGGGTC TTATCTCGGT TACACCTGTA ATCTCAGCCC TTGGGAGCCC AGAGCAGGAT	839						
146								
147	TGCTGAATGG TCTGGAGCAG GTCGTCTCGT TCCAGTCGAC	879						
148								
149	(2) INFORMATION FOR SEQ ID NO:2:							
150								
151	(i) SEQUENCE CHARACTERISTICS:							
152	(A) LENGTH: 231 amino acids							
153	(B) TYPE: amino acid							

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154 (D) TOPOLOGY: linear
155
156 (ii) MOLECULE TYPE: protein
157
158
159 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
160
161 Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu
162 1 5 10 15
163
164 Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr
165 20 25 30
166
167 Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu
168 35 40 45
169
170 Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn
171 50 55 60
172
173 Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala
174 65 70 75 80
175
176 Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln
177 85 90 95
178
179 Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys
180 100 105 110
181
182 Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile
183 115 120 125
184
185 Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
186 130 135 140
187
188 Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
189 145 150 155 160
190
191 Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
192 165 170 175
193
194 Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
195 180 185 190
196
197 Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp
198 195 200 205
199
200 Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly
201 210 215 220
202
203 Val Pro Leu Pro Ser His Pro
204 225 230

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205
206 (2) INFORMATION FOR SEQ ID NO:3:
207
208 (i) SEQUENCE CHARACTERISTICS:
209 (A) LENGTH: 24 base pairs
210 (B) TYPE: nucleic acid
211 (C) STRANDEDNESS: single
212 (D) TOPOLOGY: linear
213
214 (iii) HYPOTHETICAL: NO
215
216 (iv) ANTI-SENSE: NO
217
218 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
219

220 TCGACTGGAA CGAGACGACC TGCT

24

221
222
223 (2) INFORMATION FOR SEQ ID NO:4:
224
225 (i) SEQUENCE CHARACTERISTICS:
226 (A) LENGTH: 20 base pairs
227 (B) TYPE: nucleic acid
228 (C) STRANDEDNESS: single
229 (D) TOPOLOGY: linear
230
231 (iii) HYPOTHETICAL: NO
232
233 (iv) ANTI-SENSE: NO
234
235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
236

237 AGCAGGTCGT CTCGTTCCAG

20

238
239 (2) INFORMATION FOR SEQ ID NO:5:
240
241 (i) SEQUENCE CHARACTERISTICS:
242 (A) LENGTH: 988 base pairs
243 (B) TYPE: nucleic acid
244 (C) STRANDEDNESS: single
245 (D) TOPOLOGY: linear
246
247 (ii) MOLECULE TYPE: cDNA to mRNA
248
249 (iii) HYPOTHETICAL: NO
250
251 (iv) ANTI-SENSE: NO
252
253 (ix) FEATURE:
254 (A) NAME/KEY: CDS
255 (B) LOCATION: 30..734

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256
257      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
258
259      CGGCCGGAAT TCCGGGGCCC CCGGCCGAA ATG ACA GTG CTG GCG CCA GCC TGG      53
260                                     Met Thr Val Leu Ala Pro Ala Trp
261                                     1                               5
262
263      AGC CCA ACA ACC TAT CTC CTC CTG CTG CTG CTG CTG AGC TCG GGA CTC      101
264      Ser Pro Thr Thr Tyr Leu Leu Leu Leu Leu Leu Ser Ser Gly Leu
265          10                               15                               20
266
267      AGT GGG ACC CAG GAC TGC TCC TTC CAA CAC AGC CCC ATC TCC TCC GAC      149
268      Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp
269          25                               30                               35                               40
270
271      TTC GCT GTC AAA ATC CGT GAG CTG TCT GAC TAC CTG CTT CAA GAT TAC      197
272      Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr
273          45                               50                               55
274
275      CCA GTC ACC GTG GCC TCC AAC CTG CAG GAC GAG GAG CTC TGC GGG GGC      245
276      Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly
277          60                               65                               70
278
279      CTC TGG CGG CTG GTC CTG GCA CAG CGC TGG ATG GAG CGG CTC AAG ACT      293
280      Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr
281          75                               80                               85
282
283      GTC GCT GGG TCC AAG ATG CAA GGC TTG CTG GAG CGC GTG AAC ACG GAG      341
284      Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu
285          90                               95                               100
286
287      ATA CAC TTT GTC ACC AAA TGT GCC TTT CAG CCC CCC CCC AGC TGT CTT      389
288      Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu
289      105                               110                               115                               120
290
291      CGC TTC GTC CAG ACC AAC ATC TCC CGC CTC CTG CAG GAG ACC TCC GAG      437
292      Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu
293          125                               130                               135
294
295      CAG CTG GTG GCG CTG AAG CCC TGG ATC ACT CGC CAG AAC TTC TCC CGG      485
296      Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg
297          140                               145                               150
298
299      TGC CTG GAG CTG CAG TGT CAG CCC GAC TCC TCA ACC CTG CCA CCC CCA      533
300      Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro
301          155                               160                               165
302
303      TGG AGT CCC CGG CCC CTG GAG GCC ACA GCC CCG ACA GCC CCG CAG CCC      581
304      Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro
305          170                               175                               180
306

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307 CCT CTG CTC CTC CTA CTG CTG CTG CCC GTG GGC CTC CTG CTG CTG GCC 629
308 Pro Leu Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala
309 185 190 195 200
310
311 GCT GCC TGG TGC CTG CAC TGG CAG AGG ACG CGG CGG AGG ACA CCC CGC 677
312 Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg
313 205 210 215
314
315 CCT GGG GAG CAG GTG CCC CCC GTC CCC AGT CCC CAG GAC CTG CTG CTT 725
316 Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu
317 220 225 230
318
319 GTG GAG CAC TGACCTGGCC AAGGCCTCAT CCTGCGGAGC CTTAAACAAC 774
320 Val Glu His
321 235
322
323 GCAGTGAGAC AGACATCTAT CATCCCATTT TACAGGGGAG GATACTGAGG CACACAGAGG 834
324
325 GGAGTCACCA GCCAGAGGAT GTATAGCCTG GACACAGAGG AAGTTGGCTA GAGGCCGGTC 894
326
327 CCTTCCTTGG GCCCCTCTCA TTCCCTCCCC AGAATGGAGG CAACGCCAGA ATCCAGCACC 954
328
329 GGCCCCATTT ACCCAACTCT GAACAAAGCC CCCG 988
330
331 (2) INFORMATION FOR SEQ ID NO:6:
332
333 (i) SEQUENCE CHARACTERISTICS:
334 (A) LENGTH: 235 amino acids
335 (B) TYPE: amino acid
336 (D) TOPOLOGY: linear
337
338 (ii) MOLECULE TYPE: protein
339
340 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
341
342 Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
343 1 5 10 15
344
345 Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
346 20 25 30
347
348 Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
349 35 40 45
350
351 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
352 50 55 60
353
354 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
355 65 70 75 80
356
357 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly

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358                               85                               90                               95
359
360 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
361                               100                               105                               110
362
363 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
364                               115                               120                               125
365
366 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
367                               130                               135                               140
368
369 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
370                               145                               150                               155                               160
371
372 Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
373                               165                               170                               175
374
375 Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu Leu Leu Leu Leu Leu Leu
376                               180                               185                               190
377
378 Pro Val Gly Leu Leu Leu Leu Ala Ala Ala Trp Cys Leu His Trp Gln
379                               195                               200                               205
380
381 Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly Glu Gln Val Pro Pro Val
382                               210                               215                               220
383
384 Pro Ser Pro Gln Asp Leu Leu Leu Val Glu His
385                               225                               230                               235
386
387 (2) INFORMATION FOR SEQ ID NO:7:
388
389     (i) SEQUENCE CHARACTERISTICS:
390         (A) LENGTH: 71 base pairs
391         (B) TYPE: nucleic acid
392         (C) STRANDEDNESS: single
393         (D) TOPOLOGY: linear
394
395     (ii) MOLECULE TYPE: cDNA to mRNA
396
397     (iii) HYPOTHETICAL: NO
398
399     (iv) ANTI-SENSE: NO
400
401
402
403
404     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
405
406 AATTGGTACC TTTGGATAAA AGAGACTACA AGGACGACGA TGACAAGACA CCTGACTGTT 60
407
408 ACTTCAGCCA C 71

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409
410 (2) INFORMATION FOR SEQ ID NO:8:
411
412 (i) SEQUENCE CHARACTERISTICS:
413 (A) LENGTH: 37 base pairs
414 (B) TYPE: nucleic acid
415 (C) STRANDEDNESS: single
416 (D) TOPOLOGY: linear
417
418 (ii) MOLECULE TYPE: cDNA to mRNA
419
420 (iii) HYPOTHETICAL: NO
421
422 (iv) ANTI-SENSE: NO
423
424
425
426
427 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
428
429 ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG
430
431
432
433

37

SEQUENCE VERIFICATION REPORT
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Line	Error	Original Text
26	Wrong application Serial Number	(A) APPLICATION NUMBER: -to be assigned-
33	Unknown or Misplaced Identifier	(C) CLASSIFICATION:
38	Unknown or Misplaced Identifier	(C) CLASSIFICATION:
43	Unknown or Misplaced Identifier	(C) CLASSIFICATION:

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SEQUENCE MISSING ITEM REPORT
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< < THERE ARE NO ITEMS MISSING > >

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SEQUENCE CORRECTION REPORT
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Line	Original Text	Corrected Text
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